

#7

T10450

1/32

SEQUENCE LISTING

<110> Lassner, Michael
 Post-Beittenmiller, Dusty
 Savidge, Beth
 Weiss, James

<120> Nucleic Acid Sequences Involved in
 Tocopherol Synthesis

<130> 17133/02/US

<140> 09/549,848

<141> 2000-04-14

<150> 60/129,899

<151> 1999-04-15

<150> 60/146,461

<151> 1999-07-30

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 Val Glu Ile Asp Lys Val Asn Lys Pro Tyr Leu Pro Leu Ala Ser Gly
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      50      55      60
Gly Arg Glu Leu His Gln Glu Lys Phe Phe Gly Val Gly Trp Asn Tyr
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Arg Leu Ile Cys Gly Met Ser Ser Ser Ser Ser Val Leu Glu Gly Lys
      85      90      95
Pro Lys Lys Asp Asp Lys Glu Lys Ser Asp Gly Val Val Val Lys Lys
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Ala Ser Trp Ile Asp Leu Tyr Leu Pro Glu Glu Val Arg Gly Tyr Ala
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Gly Ala Gly Cys Thr Ile Asn Asp Leu Leu Asp Gln Asp Ile Asp Thr
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Lys Val Asp Arg Thr Lys Leu Arg Pro Ile Ala Ser Gly Leu Leu Thr
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Trp Pro Gln Ala Phe Leu Gly Leu Thr Ile Asn Trp Gly Ala Leu Leu
      260      265      270
Gly Trp Thr Ala Val Lys Gly Ser Ile Ala Pro Ser Ile Val Leu Pro
      275      280      285
Leu Tyr Leu Ser Gly Val Cys Trp Thr Leu Val Tyr Asp Thr Ile Tyr
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Ala His Gln Asp Lys Glu Asp Asp Val Lys Val Gly Val Lys Ser Thr
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Ala Leu Arg Phe Gly Asp Asn Thr Lys Leu Trp Leu Thr Gly Phe Gly
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Thr Ala Ser Ile Gly Phe Leu Ala Leu Ser Gly Phe Ser Ala Asp Leu
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Gly Trp Gln Tyr Tyr Ala Ser Leu Ala Ala Ala Ser Gly Gln Leu Gly
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Trp Gln Ile Gly Thr Ala Asp Leu Ser Ser Gly Ala Asp Cys Ser Arg
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Ser	Ser	Arg	Val	Ala	Ala	Leu	Ala	Gly	Leu	Gly	His	His	Tyr	Ala	Arg
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Pro	His	Ala	Val	Ala	Trp	Ala	Thr	Ile	Ala	Gly	Ala	Ser	Gly	Ala	Cys
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225					230					235					240
Leu	Gly	Trp	Ala	Ala	Ala	Ser	Gly	Gln	Ile	Ser	Tyr	Asn	Ser	Met	Ile
			245						250					255	

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 Ala His Leu Cys Arg Asn Asp Tyr Ala Ala Gly Gly Tyr Lys Met Leu
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 Ser Gly Leu Leu Leu His Arg Val Ser Asn Asp Asn Gln Gln Gln Leu
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 Val Glu Glu Ala Gly Leu Thr Asn Ser Val Ser Gly Glu Val Lys Thr
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 85 90 95
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 145 150 155 160
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 165 170 175
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 Ala Ser Leu Gly Lys Gly Ser Leu Ser Asp Ile Arg His Gly Val Ile
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 Val Val Asp Gln Val Glu Lys Asp Pro Arg Asn Val Asp Ile Ala Leu
 225 230 235 240
 Glu Tyr Leu Gly Lys Ser Lys Gly Ile Gln Arg Ala Arg Glu Leu Ala
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35 40 45
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50 55 60
Ile Ala Glu Ile Thr Glu Met Ile His Val Ala Ser Leu Leu His Asp
65 70 75 80
Asp Val Leu Asp Asp Ala Asp Thr Arg Arg Gly Val Gly Ser Leu Asn
85 90 95
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Gln Lys Thr Tyr Tyr Lys Thr Ala Ser Leu Ile Ser Asn Ser Cys Lys
165 170 175
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Phe Glu Tyr Gly Arg Asn Leu Gly Leu Ala Phe Gln Leu Ile Asp Asp
195 200 205
Ile Leu Asp Phe Thr Gly Thr Ser Ala Ser Leu Gly Lys Gly Ser Leu
210 215 220
Ser Asp Ile Arg His Gly Val Ile Thr Ala Pro Ile Leu Phe Ala Met
225 230 235 240
Glu Glu Phe Pro Gln Leu Arg Glu Val Val Asp Gln Val Glu Lys Asp
245 250 255
Pro Arg Asn Val Asp Ile Ala Leu Glu Tyr Leu Gly Lys Ser Lys Gly
260 265 270
Ile Gln Arg Ala Arg Glu Leu Ala Met Glu His Ala Asn Leu Ala Ala
275 280 285
Ala Ala Ile Gly Ser Leu Pro Glu Thr Asp Asn Glu Asp Val Lys Arg
290 295 300
Ser Arg Arg Ala Leu Ile Asp Leu Thr His Arg Val Ile Thr Arg Asn
305 310 315 320
Lys

```

```

<210> 13
<211> 621

```

212> DNA

<213> Arabidopsis sp

<400> 13

gctttctcct	ttgctaattc	ttgagctttc	ttgatccac	cgcgatttct	aactatttca	60
atcgcttctt	caagcgatcc	aggctcacia	aactcagact	caatgatctc	tcttagcctt	120
ggctcattct	ctagcgcgaa	gatcactggc	gccgttatgt	tacctttggc	taagtcatta	180
gctgcaggct	tacctaactg	ctctgtggac	tgagtgaagt	ccagaatgtc	atcaactact	240
tgaaaagata	aaccgagatt	cttcccgaac	tgatacattt	gctctgcgac	cttgctttcg	300
actttactga	aaattgctgc	tcctttgggtg	cttgagctga	ctaataaagc	tgtctttag	360
taactcttta	gcatgtagtc	atcaagcttg	acatcacat	cgaataaact	cgatgcttgc	420
tttatctcac	cgcttgcaaa	atctttgatc	acctgcaaaa	agataaatca	agattcagac	480
caaattgtct	ttgtattgag	tagcttcac	taattctcaga	aaggaatatt	acctgactta	540
tgagcttaat	gacttcaagg	tttctgagat	ttgtaagtac	catgatgctt	gagcaacatg	600
aaatccccag	ctaatacagc	t				621

<210> 14

<211> 741

<212> DNA

<213> Arabidopsis sp

<400> 14

ggtgagtttt	gttaatatgt	atgagattca	tctatttttg	tcataaaatt	gtttggtttg	60
gtttaaactc	tggtataaat	tgacaggaaag	gaaacagttc	atgagctttt	cggcacaaga	120
gtagcgggtg	tagctggaga	tttcatgttt	gctcaagcgt	catggtactt	agcaaatctc	180
gagaatcttg	aagttattaa	gctcatcagt	caggtactta	gttactctta	cattgttttt	240
ctatgagggt	gagctatgaa	tctcatttctg	ttgaataatg	ctgtgcctca	aacttttttt	300
catgttttca	ggtgatcaaa	gactttgcaa	gcggagagat	aaagcaggcg	tccagcttat	360
ttgactgcga	caccaagctc	gacgagtact	tactcaaaag	tttctacaag	acagcctctt	420
tagtggtctg	gagcaccaaa	ggagctgcca	ttttcagcag	agttgagcct	gatgtgacag	480
aacaaatgta	cgagtttggtg	aagaatctcg	gtctctcttt	ccagatagtt	gatgatattt	540
tggatttcac	tcagtcgaca	gagcagctcg	ggaagccagc	agggagtgtg	ttggctaaaag	600
gtaacttaac	agcactgtg	attttcgctc	tggagaggga	gccaaaggcta	agagagatca	660
ttgagtcaaa	gttctgtgag	gcgggttctc	tggaaagaagc	gattgaagcg	gtgacaaaag	720
gtggggggat	taagagagca	c				741

<210> 15

<211> 1087

<212> DNA

<213> Arabidopsis sp

<400> 15

cctcttcagc	caatccagag	gaagaagaga	caacttttta	tctttcgtca	agagtctccg	60
aaaacgcacg	gttttatgct	ctctcttctg	ccctcacctc	acaagacgca	gggcacatga	120
ttcaaccaga	gggaaaaagc	aacgataaca	actctgcttt	tgatttcaag	ctgtatatga	180
tccgcaaaagc	cgagtctgta	aatgcggctc	tcgacgtttc	cgtaccgctt	ctgaaacccc	240
ttacgatcca	agaagcggtc	aggtactctt	tgctagccgg	cggaaaaacgt	gtgaggcctc	300
tgctctgcat	tgccgcttgt	gagcttgtgg	ggggcgacga	ggctactgcc	atgtcagccg	360
cttgccgggt	cgagatgac	cacacaagct	ctctcattca	tgacgatctt	ccgtgcatgg	420
acaatgccga	cctccgtaga	ggcaagccca	ccaatcacaa	ggtatgttgt	ttaattatat	480
gaaggctcag	agataatgct	gaactagtgt	tgaaccaatt	tttgctcaaa	caaggatat	540
ggagaagaca	tggcggtttt	ggcagggtgt	gcactccttg	cattggcgtt	tgagcacatg	600
acggtttgtg	cgagtgggtt	ggtcgctccc	gagaagatga	ttcgcccggt	ggttgagctg	660
gccaggggcca	tagggactac	agggctagtt	gctggacaaa	tgatagacct	agccagcgaa	720
agactgaatc	cagacaaggt	tggattggag	catctagagt	tcacccatct	ccacaaaacg	780
gcggcattgt	tggaggcagc	ggcagtttta	ggggttataa	tgggaggtgg	aacagaggaa	840
gaaatcgaaa	agcttagaaa	gtatgctagg	tgtattggac	tactgtttca	ggttgttgat	900
gacattctcg	acgtaacaaa	atctactgag	gaattgggta	agacagccgg	aaaagacgta	960
atggccggaa	agctgacgta	tccaaggctg	ataggttttg	agggatccag	ggaagttgca	1020
gagcacctga	ggagagaagc	agaggaaaag	cttaaagggt	ttgatccaag	tcaggcggcg	1080
cctctg						1087

<210> 16

<211> 1164

<212> DNA

<213> Arabidopsis sp


```

<400> 16
atgacttcga ttctcaacac tgtctocacc atccactctt ccagagttac ctccgctgat      60
cgagtcggag tcctctctct tcggaattcg gattccggtg agttcactcg ccggcggttct      120
ggtttctcga cgttgatcta cgaatcacc cctgacaagg caccagccgg tggttcaagc      180
actgatactg ataaagttaa atctcagaca cctgacaagg caccagccgg tggttcaagc      240
attaaccagc ttctcgggtat caaaggagca tctcaagaaa ctaataaatg gaagattcgt      300
cttcagctta caaaaccagt cacttggcct ccactgggtt ggggagtcgt ctgtggtgct      360
gctgcttcag ggaactttca ttggacccca gaggatgttg ctaagtcgat tctttgcatg      420
atgatgtctg gtccttgtct tactggctat acacagacaa tcaacgactg gtatgataga      480
gatatcgacg caattaatga gccatatcgt ccaattccat ctggagcaat atcagagcca      540
gaggttatta cacaagtctg ggtgctatta ttgggaggtc ttggtattgc tggaaatatta      600
gatgtgtggg cagggcatac cactcccact gtcttctatc ttgctttggg aggatcattg      660
ctatcttata tatactctgc tccacctctt aagctaaaac aaaatggatg ggttggaat      720
tttgcaactg gagcaagcta tattagtttg ccatgggtgg ctggccaagc attggttggc      780
actcttacgc cagatgttgt tgttctaaca ctctgtgaca gcatagctgg gttaggata      840
gccattgtta acgacttcaa aagtgttgaa ggagatagag cattaggact tcagtctctc      900
ccagtagctt ttggcaccga aactgcaaaa tggatatgcg ttggtgctat agacattact      960
cagctttctg ttgccggata tctattagca tctgggaaac cttattatgc gttggcggtg     1020
gttgctttga tcattcctca gattgtgttc cagtttaaat actttctcaa ggaccctgtc     1080
aaatacgacg tcaagtacca ggcaagcgcg cagccattct tgggtgctcg aatatttgta     1140
acggcattag catcgcaaca ctga                                             1164

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<210> 17
<211> 387
<212> PRT
<213> Arabidopsis sp

```

```

<400> 17
Met Thr Ser Ile Leu Asn Thr Val Ser Thr Ile His Ser Ser Arg Val
 1          5          10          15
Thr Ser Val Asp Arg Val Gly Val Leu Ser Leu Arg Asn Ser Asp Ser
 20          25          30
Val Glu Phe Thr Arg Arg Arg Ser Gly Phe Ser Thr Leu Ile Tyr Glu
 35          40          45
Ser Pro Gly Arg Arg Phe Val Val Arg Ala Ala Glu Thr Asp Thr Asp
 50          55          60
Lys Val Lys Ser Gln Thr Pro Asp Lys Ala Pro Ala Gly Gly Ser Ser
 65          70          75          80
Ile Asn Gln Leu Leu Gly Ile Lys Gly Ala Ser Gln Glu Thr Asn Lys
 85          90          95
Trp Lys Ile Arg Leu Gln Leu Thr Lys Pro Val Thr Trp Pro Pro Leu
 100         105         110
Val Trp Gly Val Val Cys Gly Ala Ala Ser Gly Asn Phe His Trp
 115         120         125
Thr Pro Glu Asp Val Ala Lys Ser Ile Leu Cys Met Met Met Ser Gly
 130         135         140
Pro Cys Leu Thr Gly Tyr Thr Gln Thr Ile Asn Asp Trp Tyr Asp Arg
 145         150         155         160
Asp Ile Asp Ala Ile Asn Glu Pro Tyr Arg Pro Ile Pro Ser Gly Ala
 165         170         175
Ile Ser Glu Pro Glu Val Ile Thr Gln Val Trp Val Leu Leu Leu Gly
 180         185         190
Gly Leu Gly Ile Ala Gly Ile Leu Asp Val Trp Ala Gly His Thr Thr
 195         200         205
Pro Thr Val Phe Tyr Leu Ala Leu Gly Gly Ser Leu Leu Ser Tyr Ile
 210         215         220
Tyr Ser Ala Pro Pro Leu Lys Leu Lys Gln Asn Gly Trp Val Gly Asn
 225         230         235         240
Phe Ala Leu Gly Ala Ser Tyr Ile Ser Leu Pro Trp Trp Ala Gly Gln
 245         250         255
Ala Leu Phe Gly Thr Leu Thr Pro Asp Val Val Val Leu Thr Leu Leu
 260         265         270
Tyr Ser Ile Ala Gly Leu Gly Ile Ala Ile Val Asn Asp Phe Lys Ser
 275         280         285
Val Glu Gly Asp Arg Ala Leu Gly Leu Gln Ser Leu Pro Val Ala Phe
 290         295         300

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10/32

Gly Thr Glu Thr Ala Lys Trp Ile Cys Val Gly Ala Ile Asp Ile Thr
 305 310 315 320
 Gln Leu Ser Val Ala Gly Tyr Leu Leu Ala Ser Gly Lys Pro Tyr Tyr
 325 330 335
 Ala Leu Ala Leu Val Ala Leu Ile Ile Pro Gln Ile Val Phe Gln Phe
 340 345 350
 Lys Tyr Phe Leu Lys Asp Pro Val Lys Tyr Asp Val Lys Tyr Gln Ala
 355 360 365
 Ser Ala Gln Pro Phe Leu Val Leu Gly Ile Phe Val Thr Ala Leu Ala
 370 375 380
 Ser Gln His
 385

<210> 18
 <211> 981
 <212> DNA
 <213> Arabidopsis sp

<400> 18
 atgtttgttta gtggttcagc gatccatta agcagcttct gctctcttcc ggagaaaccc 60
 cacactcttc ctatgaaact ctctcccgcg gcaatccgat cttcatcctc atctgccccg 120
 ggggtcgttga acttcgatct gaggacgtat tggacgactc tgatcaccga gatcaaccag 180
 aagctggatg aggccatacc ggtcaagcac cctgcgggga tctacgaggc tatgagatac 240
 tctgtactcg cacaaggcgc caagcgtgcc cctcctgtga tgtgtgtggc ggcctgcgag 300
 ctcttcggtg gcgatcgct cgccgcttcc cccaccgcct gtgccctaga aatggtgcac 360
 gcggtctcgt tgatacacga cgacctcccc tgtatggacg acgatcctgt gcgcagagga 420
 aagccatcta accacactgt ctacggctct ggcatggcca ttctcgccgg tgacgccctc 480
 ttccactcgc cttccagca cattgtctcc cacacgcctc ctgacctgt tccccgagcc 540
 accatcctca gactcatcac tgagattgcc cgactgtcg gctccactgg tatggctgca 600
 ggccagtacg tcgaccttga aggaggtccc ttctctctt cctttgttca ggagaagaaa 660
 ttcggagcca tgggtgaatg ctctgccgtg tgcggtggcc tattggcgcg tgccactgag 720
 gatgagctcc agagtctccg aaggtagcgg agagccgtcg ggatgctgta tcaggtggtc 780
 gatgacatca ccgaggacaa gaagaagagc tatgatggtg gagcagagaa gggaatgatg 840
 gaaatggcgg aagagctcaa ggagaaggcg aagaaggagc ttcaagtgtt tgacaacaag 900
 tatggaggag gagacacact tgttcctctc tacaccttcg ttgactacgc tgctcatcga 960
 cattttcttc ttcccctctg a 981

<210> 19
 <211> 245
 <212> DNA
 <213> GLycine sp

<400> 19
 gcaacatctg ggactgggtt tgtcttgggg agtggtagt ctgttgatct ttcggcactt 60
 tcttgacttt gcttgggtac catgatggtt gctgcactct ctaactcttt gaatcaggtg 120
 tttgagatca ataattgatg taaaatgaag agaacaagtc gcaggccact accctcagga 180
 cgcatacaca tacctcatgc agttggctgg gcatcctctg ttggattagc tggtagcgct 240
 ctact 245

<210> 20
 <211> 253
 <212> DNA
 <213> Glycine sp

<400> 20
 attggttttc caagatcatt gggttttctt gttgcattca tgaccttcta ctccttgggt 60
 ttggcattgt ccaaggatat acctgacgtt gaaggagata aagagcacgg cattgattct 120
 tttgcagtac gtctaggta gaaacgggca ttttgattt gcgtttcctt ttttgaaatg 180
 gctttcggag ttggtatcct ggccggagca tcatgctcac acttttggac taaaattttc 240
 acgggtatgg gaa 253

<210> 21
 <211> 275
 <212> DNA
 <213> Glycine sp

```

<400> 21
tgatcttcta ctctctgggt atggcattgt ccaaggatat atctgacgtt aaaggagata      60
aagcatacgg catcgatact ttagcgatac gtttgggtca aaaatgggta ttttggattt      120
gcattatcct ttttgaaatg gcttttggag ttgccctctt ggcaggagca acatcttctt      180
acctttggat taaaattgtc acgggtctgg gacatgctat tcttgcttca attctcttgt      240
accaagccaa atctatatac ttgagcaaca aagtt                                     275

```

```

<210> 22
<211> 299
<212> DNA
<213> Glycine sp

```

```

<220>
<221> misc_feature
<222> (1)...(299)
<223> n = A,T,C or G

```

```

<400> 22
ccanaatang tncatcttng aaagacaatt ggcctcttca acacacaagt ctgcatgtga      60
agaagaggcc aattgtcttt ccaagatcac ttatngtggc tattgtaatc atgaacttct      120
tctttgtggg tatggcattg gcaaaggata tacctanctg ttgaaggaga taaaatatat      180
ggcattgata cttttgcaat acgtataggt caaaaacaag tattttggat ttgtattttc      240
ctttttgaaa ggctttcgga gtttccctag tggcaggagc aacatcttct agccttgggt      299

```

```

<210> 23
<211> 767
<212> DNA
<213> Glycine sp

```

```

<400> 23
gtggaggctg tgggttgctgc cctgtttatg aatatttata ttgttggttt gaatcaattg      60
tctgatgttg aaatagacaa gataaacaag ccgtatcttc cattagcadc tggggaatat      120
tcctttgaaa ctggtgtcac tattgttgca tctttttcaa ttctgagttt ttggcttggc      180
tgggtttagt gttcatggcc attatttttg gccctttttg taagctttgt gctaggaaact      240
gcttattcaa tcaatgtgcc tctgttgaga tggaaagggt ttgcagtgtc tgcagcgatg      300
tgcattctag ctgttcgggc agtaatatgt caacttgcac ttttccttca catgcagact      360
catgtgtaca agaggccacc tgtcttttca agaccattga tttttgctac tgcattcatg      420
agcttcttct ctgtagttat agcactgttt aaggatatac ctgacattga aggagataaa      480
gtatttggca tccaatcttt ttcagtgtgt ttaggtcaga agccggtggt ctggacttgt      540
gttacccttc ttgaaatagc ttatggagtc gccctcctgg tgggagctgc atctccttgt      600
ctttggagca aaattttcac ggggtctggga cacgctgtgc tggcttcaat tctctggttt      660
catgccaaat ctgtagattt gaaaagcaaa gcttcgataa catccttcta tatgtttatt      720
tggaagctat tttatgcaga atacttactc attccttttg ttagatg                                     767

```

```

<210> 24
<211> 255
<212> PRT
<213> Glycine sp

```

```

<400> 24
Val Glu Ala Val Val Ala Ala Leu Phe Met Asn Ile Tyr Ile Val Gly
1      5      10      15
Leu Asn Gln Leu Ser Asp Val Glu Ile Asp Lys Ile Asn Lys Pro Tyr
20     25     30
Leu Pro Leu Ala Ser Gly Glu Tyr Ser Phe Glu Thr Gly Val Thr Ile
35     40     45
Val Ala Ser Phe Ser Ile Leu Ser Phe Trp Leu Gly Trp Val Val Gly
50     55     60
Ser Trp Pro Leu Phe Trp Ala Leu Phe Val Ser Phe Val Leu Gly Thr
65     70     75     80
Ala Tyr Ser Ile Asn Val Pro Leu Leu Arg Trp Lys Arg Phe Ala Val
85     90     95
Leu Ala Ala Met Cys Ile Leu Ala Val Arg Ala Val Ile Val Gln Leu
100    105    110
Ala Phe Phe Leu His Met Gln Thr His Val Tyr Lys Arg Pro Pro Val

```

```

Phe Ser Arg Pro Leu Ile Phe Ala Thr Ala Phe Met Ser Phe Phe Ser
130      135      140
Val Val Ile Ala Leu Phe Lys Asp Ile Pro Asp Ile Glu Gly Asp Lys
145      150      155      160
Val Phe Gly Ile Gln Ser Phe Ser Val Cys Leu Gly Gln Lys Pro Val
165      170      175
Phe Trp Thr Cys Val Thr Leu Leu Glu Ile Ala Tyr Gly Val Ala Leu
180      185      190
Leu Val Gly Ala Ala Ser Pro Cys Leu Trp Ser Lys Ile Phe Thr Gly
195      200      205
Leu Gly His Ala Val Leu Ala Ser Ile Leu Trp Phe His Ala Lys Ser
210      215      220
Val Asp Leu Lys Ser Lys Ala Ser Ile Thr Ser Phe Tyr Met Phe Ile
225      230      235      240
Trp Lys Leu Phe Tyr Ala Glu Tyr Leu Leu Ile Pro Phe Val Arg
245      250      255

```

```

<210> 25
<211> 360
<212> DNA
<213> Zea sp

```

```

<220>
<221> misc_feature
<222> (1)...(360)
<223> n = A,T,C or G

```

```

<400> 25
ggcgtcttca cttgttctgg tcttctcgta tcccctgatg aagaggttca cattttggcc      60
tcaggcttat cttggcctga cattcaactg gggagcttta ctagggtggg ctgctattaa      120
ggaaagcata gacctgcaa atcatccttc cattgtatac agctggtatt tggtggacgc      180
tggtgtatga tactatatat gcgcatacagg tgtttcgcta tccctacttt catattaatc      240
cttgatgaag tggccatttc atgttgcgc ggtggtctta tacttgcata tctccatgca      300
tctcaggaca aagangatga cctgaaagta ggagtccaag tccacagctt aagatttggg      360

```

```

<210> 26
<211> 299
<212> DNA
<213> Zea sp

```

```

<220>
<221> misc_feature
<222> (1)...(299)
<223> n = A,T,C or G

```

```

<400> 26
gatggttgca gcatctgcaa ataccctcaa ccagggtgtt gngataaaaa atgatgctaa      60
aatgaaaagg acaatgcgtg cccctgcca tctggtcgca ttagtcctgc acatgctgcg      120
atgtgggcta caagtgttg agttgcagga acagctttgt tggcctggaa ggctaattggc      180
ttggcagctg ggcttgacgc ttctaattct gttctgtatg catttgtgta tacgccgttg      240
aagcaaatac accctgttaa tacatggggt ggggcagtcg ttggtgccat cccaccact      299

```

```

<210> 27
<211> 255
<212> DNA
<213> Zea sp

```

```

<220>
<221> misc_feature
<222> (1)...(255)
<223> n = A,T,C or G

```

```

<400> 27
anacttgc atctccatgc ntctcaggac aaagangatg acctgaaagt aggtgtcaag      60
tccacagcat taagatttgg agatttgacc nnatactgna tcagtggctt tggcgcggca      120
tgcttcggca gcttagcact cagtgggttac aatgctgacc ttggttggtg tttagtgtga      180

```

tgcttgagcg aagaatggta tngtttttac ttgatattga ctccagacct gaaatcatgt 240
 tggacagggt ggccc 255

<210> 28
 <211> 257
 <212> DNA
 <213> Zea sp

<400> 28
 attgaagggg ataggactct ggggcttcag tcacttcctg ttgcttttgg gatggaaact 60
 gcaaaatgga tttgtgttgg agcaattgat atcactcaat tatctgttgc aggttaccta 120
 ttgagcaccg gtaagctgta ttatgccctg gtgttgcttg ggctaacaat tcctcagggtg 180
 ttctttcagt tccagtactt cctgaaggac cctgtgaagt atgatgtcaa atatcaggca 240
 agcgcacaa cattctt 257

<210> 29
 <211> 368
 <212> DNA
 <213> Zea sp

<400> 29
 atccagttgc aaataataat ggcgtttctt tctgttgtaa tagcactatt caaggatata 60
 cctgacatcg aaggggaccg catattcggg atccgatcct tcagcgtccg gttagggcaa 120
 aagaaggctt tttggatctg cgttggttggt cttgagatgg cctacagcgt tgcgatactg 180
 atgggagcta cctcttctct tttgtggagc aaaacagcaa ccatcgctgg ccattccata 240
 cttgccgcga tcctatggag ctgcgcgcga tcggtggact tgacgagcaa agccgcaata 300
 acgtccttct acatgttcat ctggaagctg ttctacgcgg agtacctgct catcctctg 360
 gtgcggtg 368

<210> 30
 <211> 122
 <212> PRT
 <213> Zea sp

<400> 30
 Ile Gln Leu Gln Ile Ile Met Ala Phe Phe Ser Val Val Ile Ala Leu
 1 5 10 15
 Phe Lys Asp Ile Pro Asp Ile Glu Gly Asp Arg Ile Phe Gly Ile Arg
 20 25 30
 Ser Phe Ser Val Arg Leu Gly Gln Lys Lys Val Phe Trp Ile Cys Val
 35 40 45
 Gly Leu Leu Glu Met Ala Tyr Ser Val Ala Ile Leu Met Gly Ala Thr
 50 55 60
 Ser Ser Cys Leu Trp Ser Lys Thr Ala Thr Ile Ala Gly His Ser Ile
 65 70 75 80
 Leu Ala Ala Ile Leu Trp Ser Cys Ala Arg Ser Val Asp Leu Thr Ser
 85 90 95
 Lys Ala Ala Ile Thr Ser Phe Tyr Met Phe Ile Trp Lys Leu Phe Tyr
 100 105 110
 Ala Glu Tyr Leu Leu Ile Pro Leu Val Arg
 115 120

<210> 31
 <211> 278
 <212> DNA
 <213> Zea sp

<400> 31
 tattcagcac cacctctcaa gctcaagcag aatggatgga ttgggaactt cgctctgggt 60
 gcgagttaca tcagcttgcc ctggtgggct ggccaggcgt tatttggaac tcttacacca 120
 gatatacatt tcttgactac tttgtacagc atagctgggc tagggattgc tattgtaaat 180
 gatttcaaga gtattgaagg ggataggact ctggggcttc agtcacttcc tgttgctttt 240
 gggatggaaa ctgcaaaatg gatttgtgtt ggagcaat 278

<210> 32
 <211> 292

<212> PRT

<213> Synechocystis sp

<400> 32

```

Met Val Ala Gln Thr Pro Ser Ser Pro Pro Leu Trp Leu Thr Ile Ile
 1          5          10          15
Tyr Leu Leu Arg Trp His Lys Pro Ala Gly Arg Leu Ile Leu Met Ile
 20          25          30
Pro Ala Leu Trp Ala Val Cys Leu Ala Ala Gln Gly Leu Pro Pro Leu
 35          40          45
Pro Leu Leu Gly Thr Ile Ala Leu Gly Thr Leu Ala Thr Ser Gly Leu
 50          55          60
Gly Cys Val Val Asn Asp Leu Trp Asp Arg Asp Ile Asp Pro Gln Val
 65          70          75          80
Glu Arg Thr Lys Gln Arg Pro Leu Ala Ala Arg Ala Leu Ser Val Gln
 85          90          95
Val Gly Ile Gly Val Ala Leu Val Ala Leu Leu Cys Ala Ala Gly Leu
 100         105         110
Ala Phe Tyr Leu Thr Pro Leu Ser Phe Trp Leu Cys Val Ala Ala Val
 115         120         125
Pro Val Ile Val Ala Tyr Pro Gly Ala Lys Arg Val Phe Pro Val Pro
 130         135         140
Gln Leu Val Leu Ser Ile Ala Trp Gly Phe Ala Val Leu Ile Ser Trp
 145         150         155         160
Ser Ala Val Thr Gly Asp Leu Thr Asp Ala Thr Trp Val Leu Trp Gly
 165         170         175
Ala Thr Val Phe Trp Thr Leu Gly Phe Asp Thr Val Tyr Ala Met Ala
 180         185         190
Asp Arg Glu Asp Asp Arg Arg Ile Gly Val Asn Ser Ser Ala Leu Phe
 195         200         205
Phe Gly Gln Tyr Val Gly Glu Ala Val Gly Ile Phe Phe Ala Leu Thr
 210         215         220
Ile Gly Cys Leu Phe Tyr Leu Gly Met Ile Leu Met Leu Asn Pro Leu
 225         230         235         240
Tyr Trp Leu Ser Leu Ala Ile Ala Ile Val Gly Trp Val Ile Gln Tyr
 245         250         255
Ile Gln Leu Ser Ala Pro Thr Pro Glu Pro Lys Leu Tyr Gly Gln Ile
 260         265         270
Phe Gly Gln Asn Val Ile Ile Gly Phe Val Leu Leu Ala Gly Met Leu
 275         280         285
Leu Gly Trp Leu
 290

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<210> 33

<211> 316

<212> PRT

<213> Synechocystis sp

<400> 33

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Met Val Thr Ser Thr Lys Ile His Arg Gln His Asp Ser Met Gly Ala
 1          5          10          15
Val Cys Lys Ser Tyr Tyr Gln Leu Thr Lys Pro Arg Ile Ile Pro Leu
 20          25          30
Leu Leu Ile Thr Thr Ala Ala Ser Met Trp Ile Ala Ser Glu Gly Arg
 35          40          45
Val Asp Leu Pro Lys Leu Leu Ile Thr Leu Leu Gly Gly Thr Leu Ala
 50          55          60
Ala Ala Ser Ala Gln Thr Leu Asn Cys Ile Tyr Asp Gln Asp Ile Asp
 65          70          75          80
Tyr Glu Met Leu Arg Thr Arg Ala Arg Pro Ile Pro Ala Gly Lys Val
 85          90          95
Gln Pro Arg His Ala Leu Ile Phe Ala Leu Ala Leu Gly Val Leu Ser
 100         105         110
Phe Ala Leu Leu Ala Thr Phe Val Asn Val Leu Ser Gly Cys Leu Ala
 115         120         125

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Leu Ser Gly Ile Val Phe Tyr Met Leu Val Tyr Thr His Trp Leu Lys
 130 135 140
 Arg His Thr Ala Gln Asn Ile Val Ile Gly Gly Ala Ala Gly Ser Ile
 145 150 155 160
 Pro Pro Leu Val Gly Trp Ala Ala Val Thr Gly Asp Leu Ser Trp Thr
 165 170 175
 Pro Trp Val Leu Phe Ala Leu Ile Phe Leu Trp Thr Pro Pro His Phe
 180 185 190
 Trp Ala Leu Ala Leu Met Ile Lys Asp Asp Tyr Ala Gln Val Asn Val
 195 200 205
 Pro Met Leu Pro Val Ile Ala Gly Glu Glu Lys Thr Val Ser Gln Ile
 210 215 220
 Trp Tyr Tyr Ser Leu Leu Val Val Pro Phe Ser Leu Leu Leu Val Tyr
 225 230 235 240
 Pro Leu His Gln Leu Gly Ile Leu Tyr Leu Ala Ile Ala Ile Ile Leu
 245 250 255
 Gly Gly Gln Phe Leu Val Lys Ala Trp Gln Leu Lys Gln Ala Pro Gly
 260 265 270
 Asp Arg Asp Leu Ala Arg Gly Leu Phe Lys Phe Ser Ile Phe Tyr Leu
 275 280 285
 Met Leu Leu Cys Leu Ala Met Val Ile Asp Ser Leu Pro Val Thr His
 290 295 300
 Gln Leu Val Ala Gln Met Gly Thr Leu Leu Leu Gly
 305 310 315

<210> 34

<211> 324

<212> PRT

<213> Synechocystis sp

<400> 34

Met Ser Asp Thr Gln Asn Thr Gly Gln Asn Gln Ala Lys Ala Arg Gln
 1 5 10 15
 Leu Leu Gly Met Lys Gly Ala Ala Pro Gly Glu Ser Ser Ile Trp Lys
 20 25 30
 Ile Arg Leu Gln Leu Met Lys Pro Ile Thr Trp Ile Pro Leu Ile Trp
 35 40 45
 Gly Val Val Cys Gly Ala Ala Ser Ser Gly Gly Tyr Ile Trp Ser Val
 50 55 60
 Glu Asp Phe Leu Lys Ala Leu Thr Cys Met Leu Leu Ser Gly Pro Leu
 65 70 75 80
 Met Thr Gly Tyr Thr Gln Thr Leu Asn Asp Phe Tyr Asp Arg Asp Ile
 85 90 95
 Asp Ala Ile Asn Glu Pro Tyr Arg Pro Ile Pro Ser Gly Ala Ile Ser
 100 105 110
 Val Pro Gln Val Val Thr Gln Ile Leu Ile Leu Leu Val Ala Gly Ile
 115 120 125
 Gly Val Ala Tyr Gly Leu Asp Val Trp Ala Gln His Asp Phe Pro Ile
 130 135 140
 Met Met Val Leu Thr Leu Gly Gly Ala Phe Val Ala Tyr Ile Tyr Ser
 145 150 155 160
 Ala Pro Pro Leu Lys Leu Lys Gln Asn Gly Trp Leu Gly Asn Tyr Ala
 165 170 175
 Leu Gly Ala Ser Tyr Ile Ala Leu Pro Trp Trp Ala Gly His Ala Leu
 180 185 190
 Phe Gly Thr Leu Asn Pro Thr Ile Met Val Leu Thr Leu Ile Tyr Ser
 195 200 205
 Leu Ala Gly Leu Gly Ile Ala Val Val Asn Asp Phe Lys Ser Val Glu
 210 215 220
 Gly Asp Arg Gln Leu Gly Leu Lys Ser Leu Pro Val Met Phe Gly Ile
 225 230 235 240
 Gly Thr Ala Ala Trp Ile Cys Val Ile Met Ile Asp Val Phe Gln Ala
 245 250 255
 Gly Ile Ala Gly Tyr Leu Ile Tyr Val His Gln Gln Leu Tyr Ala Thr
 260 265 270

Ile Val Leu Leu Leu Leu Ile Pro Gln Ile Thr Phe Gln Asp Met Tyr
 275 280 285
 Phe Leu Arg Asn Pro Leu Glu Asn Asp Val Lys Tyr Gln Ala Ser Ala
 290 295 300
 Gln Pro Phe Leu Val Phe Gly Met Leu Ala Thr Gly Leu Ala Leu Gly
 305 310 315 320
 His Ala Gly Ile

<210> 35
 <211> 307
 <212> PRT
 <213> Synechocystis sp

<400> 35
 Met Thr Glu Ser Ser Pro Leu Ala Pro Ser Thr Ala Pro Ala Thr Arg
 1 5 10 15
 Lys Leu Trp Leu Ala Ala Ile Lys Pro Pro Met Tyr Thr Val Ala Val
 20 25 30
 Val Pro Ile Thr Val Gly Ser Ala Val Ala Tyr Gly Leu Thr Gly Gln
 35 40 45
 Trp His Gly Asp Val Phe Thr Ile Phe Leu Leu Ser Ala Ile Ala Ile
 50 55 60
 Ile Ala Trp Ile Asn Leu Ser Asn Asp Val Phe Asp Ser Asp Thr Gly
 65 70 75 80
 Ile Asp Val Arg Lys Ala His Ser Val Val Asn Leu Thr Gly Asn Arg
 85 90 95
 Asn Leu Val Phe Leu Ile Ser Asn Phe Phe Leu Leu Ala Gly Val Leu
 100 105 110
 Gly Leu Met Ser Met Ser Trp Arg Ala Gln Asp Trp Thr Val Leu Glu
 115 120 125
 Leu Ile Gly Val Ala Ile Phe Leu Gly Tyr Thr Tyr Gln Gly Pro Pro
 130 135 140
 Phe Arg Leu Gly Tyr Leu Gly Leu Gly Glu Leu Ile Cys Leu Ile Thr
 145 150 155 160
 Phe Gly Pro Leu Ala Ile Ala Ala Ala Tyr Tyr Ser Gln Ser Gln Ser
 165 170 175
 Phe Ser Trp Asn Leu Leu Thr Pro Ser Val Phe Val Gly Ile Ser Thr
 180 185 190
 Ala Ile Ile Leu Phe Cys Ser His Phe His Gln Val Glu Asp Asp Leu
 195 200 205
 Ala Ala Gly Lys Lys Ser Pro Ile Val Arg Leu Gly Thr Lys Leu Gly
 210 215 220
 Ser Gln Val Leu Thr Leu Ser Val Val Ser Leu Tyr Leu Ile Thr Ala
 225 230 235 240
 Ile Gly Val Leu Cys His Gln Ala Pro Trp Gln Thr Leu Leu Ile Ile
 245 250 255
 Ala Ser Leu Pro Trp Ala Val Gln Leu Ile Arg His Val Gly Gln Tyr
 260 265 270
 His Asp Gln Pro Glu Gln Val Ser Asn Cys Lys Phe Ile Ala Val Asn
 275 280 285
 Leu His Phe Phe Ser Gly Met Leu Met Ala Ala Gly Tyr Gly Trp Ala
 290 295 300
 Gly Leu Gly
 305

<210> 36
 <211> 927
 <212> DNA
 <213> Synechocystis sp

<400> 36
 atggcaacta tccaagcttt ttggcgcttc tcccgccccc ataccatcat tgggtacaact 60
 ctgagcgtct gggctgtgta tctgttaact attctcgggg atggaaactc agttaactcc 120
 cctgcttccc tggatttagt gttcggcgct tggctggcct gcctgttggg taatgtgtac 180
 attgtcggcc tcaaccaatt gtgggatgtg gacattgacc gcatcaataa gccgaatttg 240


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cccctagcta acggagattt ttctatcgcc cagggccggt ggattgtggg actttgtggc 300
ggtgcttcct tggcgatcgc ctggggatta gggctatggc tggggctaac ggtgggcatt 360
agtttgatta ttggcacggc ctattcgggt cggccagtga ggtaaagcg cttttccctg 420
ctggcgggcc tgtgtattct gacggtgcgg ggaattgtgg ttaacttggg cttattttta 480
tttttttaga ttggtttagg ttatccccc accttaataa ccccatctg ggttttgact 540
ttatttatct tagttttcac cgtggcgatc gccattttta aagatgtgcc agatatggaa 600
ggcgatcggc aatttaagat tcaaacttta actttgcaaa tcggcaaaca aaacggtttt 660
cggggaacct taattttact cactggttgt tatttagcca tggcaatctg gggcttatgg 720
gcggctatgc ctttaaatac tgctttcttg attgtttccc atttggtgct attagcetta 780
ctctgggtggc ggagtcgaga tgtacactta gaaagcaaaa ccgaaattgc tagtttttat 840
cagtttattt ggaagctatt tttcttagag tacttgctgt atcccttggc tctgtgggta 900
cctaattttt ctaatactat ttttttag 927

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<210> 37

<211> 308

<212> PRT

<213> Synechocystis sp

<400> 37

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Met Ala Thr Ile Gln Ala Phe Trp Arg Phe Ser Arg Pro His Thr Ile
1          5          10          15
Ile Gly Thr Thr Leu Ser Val Trp Ala Val Tyr Leu Leu Thr Ile Leu
20          25          30
Gly Asp Gly Asn Ser Val Asn Ser Pro Ala Ser Leu Asp Leu Val Phe
35          40          45
Gly Ala Trp Leu Ala Cys Leu Leu Gly Asn Val Tyr Ile Val Gly Leu
50          55          60
Asn Gln Leu Trp Asp Val Asp Ile Asp Arg Ile Asn Lys Pro Asn Leu
65          70          75          80
Pro Leu Ala Asn Gly Asp Phe Ser Ile Ala Gln Gly Arg Trp Ile Val
85          90          95
Gly Leu Cys Gly Val Ala Ser Leu Ala Ile Ala Trp Gly Leu Gly Leu
100         105         110
Trp Leu Gly Leu Thr Val Gly Ile Ser Leu Ile Ile Gly Thr Ala Tyr
115         120         125
Ser Val Pro Pro Val Arg Leu Lys Arg Phe Ser Leu Leu Ala Ala Leu
130         135         140
Cys Ile Leu Thr Val Arg Gly Ile Val Val Asn Leu Gly Leu Phe Leu
145         150         155         160
Phe Phe Arg Ile Gly Leu Gly Tyr Pro Pro Thr Leu Ile Thr Pro Ile
165         170         175
Trp Val Leu Thr Leu Phe Ile Leu Val Phe Thr Val Ala Ile Ala Ile
180         185         190
Phe Lys Asp Val Pro Asp Met Glu Gly Asp Arg Gln Phe Lys Ile Gln
195         200         205
Thr Leu Thr Leu Gln Ile Gly Lys Gln Asn Val Phe Arg Gly Thr Leu
210         215         220
Ile Leu Leu Thr Gly Cys Tyr Leu Ala Met Ala Ile Trp Gly Leu Trp
225         230         235         240
Ala Ala Met Pro Leu Asn Thr Ala Phe Leu Ile Val Ser His Leu Cys
245         250         255
Leu Leu Ala Leu Leu Trp Trp Arg Ser Arg Asp Val His Leu Glu Ser
260         265         270
Lys Thr Glu Ile Ala Ser Phe Tyr Gln Phe Ile Trp Lys Leu Phe Phe
275         280         285
Leu Glu Tyr Leu Leu Tyr Pro Leu Ala Leu Trp Leu Pro Asn Phe Ser
290         295         300
Asn Thr Ile Phe
305

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<210> 38

<211> 1092

<212> DNA

<213> Synechocystis sp

<400> 38
 atgaaatttc cgccccacag tggttaccat tggcaaggtc aatcaccttt ctttgaaggt 60
 tggtagctgc gcctgctttt gccccaatcc ggggaaagtt ttgcttttat gtactccatc 120
 gaaaatcctg ctacgatca tcattacggc ggcggtgctg tgcaaatttt agggccggct 180
 acgaaaaaac aagaaaatca ggaagaccaa cttgtttggc ggacatttcc ctcggtaaaa 240
 aaattttggg ccagtcctcg ccagtttgcc ctagggcatt ggggaaaatg tagggataac 300
 aggcaggcga aacccctact ctccgaagaa ttttttgcca cggccaagga aggttatcaa 360
 atccatcaaa atcagcacca aggacaaatc attcatggcg atcgccattg tcggttggcag 420
 ttcaccgtag aaccggaagt aacttggggg agtcctaacc gatttcctcg ggctacagcg 480
 ggttggcttt cttttttacc cttgtttgat cccggttggc aaattctttt agcccaaggt 540
 agagcgcacg gctggctgaa atggcagagg gaacagtatg aatttgacca cgccctagtt 600
 tatgccgaaa aaaattgggg tcaactccttt ccctcccgtt ggttttggct ccaagcaaatt 660
 tattttcctg accatccagg actgagcgct actgcccgtg gcggggaacg gattgttctt 720
 ggtcgccccc aagaggtagc ttaattggc ttacatcacc aaggtaattt ttacgaattt 780
 ggcccgggcc atggcacagt cacttggcaa gtagctccct ggggccgttg gcaattaaaa 840
 gccagcaatg ataggtattg ggtcaagttg tccggaaaaa cagataaaaa aggcagttta 900
 gtccacactc ccaccgcccc gggcttacaa ctcaactgcc gagataccac taggggctat 960
 ttgtatttgc aattgggatc tgtgggtcac ggcctgatag tgcaagggga aacggacacc 1020
 gcggggctag aagttggagg tgattggggt ttaacagagg aaaatttgag caaaaaaaca 1080
 gtgccattct ga 1092

<210> 39
 <211> 363
 <212> PRT
 <213> Synechocystis sp

<400> 39
 Met Lys Phe Pro Pro His Ser Gly Tyr His Trp Gln Gly Gln Ser Pro
 1 5 10 15
 Phe Phe Glu Gly Trp Tyr Val Arg Leu Leu Leu Pro Gln Ser Gly Glu
 20 25 30
 Ser Phe Ala Phe Met Tyr Ser Ile Glu Asn Pro Ala Ser Asp His His
 35 40 45
 Tyr Gly Gly Gly Ala Val Gln Ile Leu Gly Pro Ala Thr Lys Lys Gln
 50 55 60
 Glu Asn Gln Glu Asp Gln Leu Val Trp Arg Thr Phe Pro Ser Val Lys
 65 70 75 80
 Lys Phe Trp Ala Ser Pro Arg Gln Phe Ala Leu Gly His Trp Gly Lys
 85 90 95
 Cys Arg Asp Asn Arg Gln Ala Lys Pro Leu Leu Ser Glu Glu Phe Phe
 100 105 110
 Ala Thr Val Lys Glu Gly Tyr Gln Ile His Gln Asn Gln His Gln Gly
 115 120 125
 Gln Ile Ile His Gly Asp Arg His Cys Arg Trp Gln Phe Thr Val Glu
 130 135 140
 Pro Glu Val Thr Trp Gly Ser Pro Asn Arg Phe Pro Arg Ala Thr Ala
 145 150 155 160
 Gly Trp Leu Ser Phe Leu Pro Leu Phe Asp Pro Gly Trp Gln Ile Leu
 165 170 175
 Leu Ala Gln Gly Arg Ala His Gly Trp Leu Lys Trp Gln Arg Glu Gln
 180 185 190
 Tyr Glu Phe Asp His Ala Leu Val Tyr Ala Glu Lys Asn Trp Gly His
 195 200 205
 Ser Phe Pro Ser Arg Trp Phe Trp Leu Gln Ala Asn Tyr Phe Pro Asp
 210 215 220
 His Pro Gly Leu Ser Val Thr Ala Ala Gly Gly Glu Arg Ile Val Leu
 225 230 235 240
 Gly Arg Pro Glu Glu Val Ala Leu Ile Gly Leu His His Gln Gly Asn
 245 250 255
 Phe Tyr Glu Phe Gly Pro Gly His Gly Thr Val Thr Trp Gln Val Ala
 260 265 270
 Pro Trp Gly Arg Trp Gln Leu Lys Ala Ser Asn Asp Arg Tyr Trp Val
 275 280 285
 Lys Leu Ser Gly Lys Thr Asp Lys Lys Gly Ser Leu Val His Thr Pro
 290 295 300

Thr Ala Gln Gly Leu Gln Leu Asn Cys Arg Asp Thr Thr Arg Gly Tyr
 305 310 315 320
 Leu Tyr Leu Gln Leu Gly Ser Val Gly His Gly Leu Ile Val Gln Gly
 325 330 335
 Glu Thr Asp Thr Ala Gly Leu Glu Val Gly Gly Asp Trp Gly Leu Thr
 340 345 350
 Glu Glu Asn Leu Ser Lys Lys Thr Val Pro Phe
 355 360

<210> 40
 <211> 56
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Oligonucleotide

<400> 40
 cgcgatttaa atggcgcgcc ctgcaggcgg ccgcctgcag ggcgcgccat ttaaat 56

<210> 41
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Oligonucleotide

<400> 41
 tcgaggatcc gcggccgcaa gcttcctgca gg 32

<210> 42
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Oligonucleotide

<400> 42
 tcgacctgca ggaagcttgc ggccgcggat cc 32

<210> 43
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Oligonucleotide

<400> 43
 tcgacctgca ggaagcttgc ggccgcggat cc 32

<210> 44
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Oligonucleotide

<400> 44
 tcgaggatcc gcggccgcaa gcttcctgca gg 32

<210> 45
 <211> 36

212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligonucleotide

 <400> 45
 tcgaggatcc gcggccgcaa gcttcctgca ggagct 36

 <210> 46
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligonucleotide

 <400> 46
 cctgcaggaa gcttgccggc gcggatcc 28

 <210> 47
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligonucleotide

 <400> 47
 tcgacctgca ggaagcttgc ggccgcggat ccagct 36

 <210> 48
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligonucleotide

 <400> 48
 ggatccgcgg ccgcaagctt cctgcagg 28

 <210> 49
 <211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligonucleotide

 <400> 49
 gatcacctgc aggaagcttg cggccgcgga tccaatgca 39

 <210> 50
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligonucleotide

 <400> 50
 ttggatccgc ggccgcaagc ttctgcagg t 31

 <210> 51
 <211> 41

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligonucleotide

 <400> 51
 ggatccgcgg ccgcacaatg gagtctctgc tctctagttc t 41

 <210> 52
 <211> 38
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligonucleotide

 <400> 52
 ggatcctgca ggtcacttca aaaaaggtaa cagcaagt 38

 <210> 53
 <211> 45
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligonucleotide

 <400> 53
 ggatccgcgg ccgcacaatg gcgttttttg ggctctcccg tgttt 45

 <210> 54
 <211> 40
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligonucleotide

 <400> 54
 ggatcctgca ggattattgaa aacttcttcc aagtacaact 40

 <210> 55
 <211> 38
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligonucleotide

 <400> 55
 ggatccgcgg ccgcacaatg tggcgaagat ctgttggt 38

 <210> 56
 <211> 37
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligonucleotide

 <400> 56
 ggatcctgca ggtcatggag agtagaagga aggagct 37

 <210> 57
 <211> 50

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligonucleotide

 <400> 57
 ggatccgcgg ccgcacaatg gtacttgccg aggttccaaa gcttgcctct 50

 <210> 58
 <211> 38
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligonucleotide

 <400> 58
 ggatcctgca ggtcacttgt ttctggatgat gactctat 38

 <210> 59
 <211> 38
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligonucleotide

 <400> 59
 ggatccgcgg ccgcacaatg acttcgattc tcaacact 38

 <210> 60
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligonucleotide

 <400> 60
 ggatcctgca ggtcagtgtt gcgatgctaa tgccgt 36

 <210> 61
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligonucleotide

 <400> 61
 taatgtgtac attgtcggcc tc 22

 <210> 62
 <211> 60
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligonucleotide

 <400> 62
 gcaatgtaac atcagagatt ttgagacaca acgtggcttt ccacaattcc ccgcaccgtc 60

 <210> 63
 <211> 22

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligonucleotide

 <400> 63
 aggctaataa gcacaaatgg ga 22

 <210> 64
 <211> 63
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligonucleotide

 <400> 64
 ggtatgagtc agcaacacct tcttcacgag gcagacctca gcggaattgg tttagggttat 60
 ccc 63

 <210> 65
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligonucleotide

 <400> 65
 ggatccatgg ttgcccaaac cccatc 26

 <210> 66
 <211> 61
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligonucleotide

 <400> 66
 gcaatgtaac atcagagatt ttgagacaca acgtggcttt gggttaagcaa caatgaccgg 60
 c 61

 <210> 67
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligonucleotide

 <400> 67
 gaattctcaa agccagccca gtaac 25

 <210> 68
 <211> 63
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligonucleotide

 <400> 68
 ggtatgagtc agcaacacct tcttcacgag gcagacctca gcgggtgcga aaagggtttt 60
 ccc 63

<210> 69
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligonucleotide

 <400> 69
 ccagtgggtt aggctgtgtg gtc 23

 <210> 70
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligonucleotide

 <400> 70
 ctgagttgga tgtattggat c 21

 <210> 71
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligonucleotide

 <400> 71
 ggatccatgg ttacttcgac aaaaatcc 28

 <210> 72
 <211> 60
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligonucleotide

 <400> 72
 gcaatgtaac atcagagatt ttgagacaca acgtggcttt gctaggcaac cgcttagtac 60

 <210> 73
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligonucleotide

 <400> 73
 gaattcttaa cccaacagta aagttccc 28

 <210> 74
 <211> 63
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligonucleotide

 <400> 74
 ggtatgagtc agcaacacct tcttcacgag gcagacctca gcgccggcat tgtcttttac 60
 atg 63

<210> 75
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligonucleotide

 <400> 75
 ggaacccttg cagccgcttc 20

 <210> 76
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligonucleotide

 <400> 76
 gtatgcccaa ctggtgcaga gg 22

 <210> 77
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligonucleotide

 <400> 77
 ggatccatgt ctgacacaca aaataccg 28

 <210> 78
 <211> 62
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligonucleotide

 <400> 78
 gcaatgtaac atcagagatt ttgagacaca acgtggcttt cgccaatacc agccaccaac 60
 ag 62

 <210> 79
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligonucleotide

 <400> 79
 gaattctcaa atccccgcatt ggcctag 27

 <210> 80
 <211> 65
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligonucleotide

<400> 80
 ggtatgagtc agcaacacct tcttcacgag gcagacctca gcggcctacg gcttggacgt 60
 gtggg 65

 <210> 81
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligonucleotide

 <400> 81
 cacttgatt cccctgatct g 21

 <210> 82
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligonucleotide

 <400> 82
 gcaatacccg cttggaaaac g 21

 <210> 83
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligonucleotide

 <400> 83
 ggatccatga ccgaatcttc gcccctagc 29

 <210> 84
 <211> 61
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligonucleotide

 <400> 84
 gcaatgtaac atcagagatt ttgagacaca acgtggcttt caatcctagg tagccgaggc 60
 g 61

 <210> 85
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligonucleotide

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<211> 4450

<212> DNA

<213> Arabidopsis sp

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